

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:32 ; Search time 170.72 Seconds

(without alignments)
248,582 Million cell updates/sec

Title: US-09-331-631A-5

Perfect score: 3326
Sequence: 1 OCMOLETSGOMRRCVSOCDK.....SPRSTKQOQPLVSTILDVFGF 625

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1163	35.0	810	2 T44430	protein PY100 (imp
2	1112	33.4	566	2 S22477	vicilin precursor
3	1074.5	32.3	588	1 FWCNAB	alpha-globulin B p
4	1063.5	32.0	605	2 S06398	alpha-globulin typ
5	1018.5	30.6	509	2 S08059	alpha-globulin typ
6	903	27.1	573	2 A53234	globulin-1S, GlB1S
7	888	26.7	582	2 B53234	vicilin-like stora
8	864.5	26.0	637	2 S35221	globulin Bgl prec
9	859.5	25.8	605	1 FWSYBA	beta-conglycinin a
10	858.5	25.8	605	2 S20007	beta-conglycinin a
11	854.5	25.7	639	2 B24810	convicilin precurs
12	833	25.0	571	2 S00566	convicilin precurs
13	794	23.9	524	2 JQ1730	62K sucrose-bindin
14	775.5	23.3	483	2 T06459	vicilin precursor
15	759.5	22.8	433	2 S00567	vicilin precursor
16	759.5	22.8	433	2 S08505	vicilin precursor
17	757.5	22.8	438	2 S35757	vicilin garden p
18	749	22.5	439	1 FWSYCB	vicilin, 47k - gar
19	740	22.2	448	1 S24756	beta-conglycinin b
20	722	21.7	450	2 S15675	vicilin-like stora
21	717.5	21.6	463	2 A27288	vicilin precursor
22	713.5	21.5	463	2 S06309	vicilin precursor
23	712.5	21.4	410	1 FWPMBV	vicilin precursor
24	692.5	20.8	445	2 JQ2264	vicilin B precursor
25	685.5	20.6	445	2 S00281	canavalin - jack b
26	563	16.9	436	2 A23498	canavalin - sword
27	560	16.8	430	2 S10156	phaseolin type alp
28	558.5	16.8	414	2 S60190	alpha-phaseolin pr
29	552	16.6	421	2 A24810	phaseolin beta cna

30	532.5	16.0	540	2 S21825	vicilin-like stora
31	414	12.4	275	1 FWPWVA	vicilin A precursor
32	368.5	11.1	236	2 T01662	globulin-1 - maize
33	365	11.0	196	2 S02281	convicilin (clone
34	365	11.0	499	2 T10443	probable major pro
35	361	10.9	296	2 T06572	convicilin precurs
36	360	10.8	407	2 T02258	globulin-1 - maize
37	356	10.7	218	2 T06399	beta-conglycinin a
38	339	10.2	240	2 T06399	7S storage prote
39	330	9.9	481	2 T14300	hypothetical prote
40	223.5	6.7	136	2 T02870	globulin 2 precurs
41	216	6.5	1898	1 A45973	trichohyalin - hum
42	213.5	6.4	184	1 FSWB	phaseolin - kidney
43	210	6.3	551	2 S51941	prunin 1 precursor
44	196.5	5.9	781	2 T02272	hypothetical prote
45	196	5.9	1407	1 S28589	trichohyalin - rab

ALIGNMENTS

RESULT 1	protein PY100 [imported] - winter squash
T44430	C:Species: Cucurbita maxima (winter squash)
	C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
	C:Accession: T44430
R:Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I.	
J. Biol. Chem. 274, 2563-2570, 1999	
A:Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin	
A:Reference number: Z22767; PMID:99107919	
A:Accession: T44430	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-810 <YAM>	
A:Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062	
Query Match	35.0%; Score 1163; DB 2; Length 810;
Best local similarity	36.8%; Pred. No. 6,1e-66;
Matches 271; Conservative 133; Mismatches 192; Indels 140; Gaps 22;	
QY 10 QMRRCVSOCDKRFEE-----DIDMSKY-----31	
DB 94 QQRKCEQVEERLREREGEDVDEVERRDPEMERERORRRERERERERER 153	
QY 32 -----DNGEDPOTECQOCQRCROESDPROOQYQCRCKELCEEEFYNNRQDPQOY 85	
DB 154 GRGRDENERDPRKEQEEEROR--REQERRRRREQEORERERGRERDEDEDEN-QRDPWRR 210	
QY 86 EGCQRRCORRETPRIMOICQORCEERY-----EKE-----KROOQRYEEQOREDE 132	
DB 211 EQ-----ERREDEERRRREQEORERERERERERERERERERERER 265	
QY 133 EYEEPMKSGDKNRDP-----QOREEDCRHRCQO-----EP--R 166	
DB 266 ERRGGRDDEDENQRDPDRREQERERRRERERERERERERERERERER 325	
QY 167 LQYQOCROEQO-----QOHGRGG-----DLNPRGGSGGRLEE-----GEKK 205	
DB 326 RQERRRREERERERERERERERERERERERERERERERERERERER 385	
QY 206 QSDNPPYFDEERSLSTRFEEGHISYLENFYGRSKLLRALKNYRLVLANNAFVLPFH 265	
DB 386 QSNPPYFQEQRFQSKYRDEGIMRWLEFSESLKIKKORLALLFARPHTPVPHH 445	
QY 266 LDADATLLVYGGRGALMLHRNR-----ESYMLECGDVIRIPAGTFYLLINDNNEERLAI 321	
DB 446 LDAECVLLVVRRAITTVVQERRETRKESYNVESGDVMTIPAGTLYLANGE-NEDLQI 504	
QY 322 AKFLQIRISPGQYKEFFPAGQNPPEYLSFTSKELALNLTOTERLKVQGOQE--GV 379	
DB 505 VLVQVPNNPCEKDYLLSAGES-QAYYVSFSDVLEALNIPKLERIFQORERGCK 563	

[illegible]

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RESULT      2
S22477
vicillin precursor - cacao
C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
R:McHenry, L.; Fritze, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A:Title: Comparison of the structure and nucleotide sequence of vicillin genes of cacao
A:Reference number: S22477; MUID:92288309
A:Accession: S22477
A:Molecule type: DNA
A:Residues: 1-566 <MC1>
A:Cross-references: EMBL:X62625
A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626
C:Genetics:
A:introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-566/Product: vicillin #status predicted <MAT>

```

Query Match	33.4%	Score 1112	DB 2	Length 566
Best Local Similarity	40.6%	Pred. No. 6.6e-63		
Matches 234	Conservative 106	Mismatches 179	Indels 58	Gaps 13

QY	68	ICEEEENR-----ORDPOOYOCOKRORETPRIMOJOCOSERYEKEKROKRY	124
Db	22	LCGSVSAWGKROYERDRPOQYEOOCRCESATPDEROEOCBOCRSE-----EY	70
QY	125	EEOOOREDEKTEEMKBSGDNKRDFOOREYEDCRHHCOD-----PRLOYOCRCOEOORON	182
Db	71	KEOORODEEL-----OROYOCOCRCOEOOOGOREOOCOCRCMEYOKEO	116
QY	183	GRCGLMPORQSGCRPECEGKSDRPPYFDE-RSLSTFRPTEEGHISYLEMNYGSKL	241
Db	117	ER-GEHEUYHNHKKNRSEEBEGGOORNNPYPFRKRSQOTFRDEEGNFKLQRFALNSPP	175
QY	242	LRLAKNRYLVLEAPNPAFVLPTHLDAIILVIGSGALMKIHRDNRESYNLECGDVR	301
Db	176	LKGINDRYALMAFENAPMPTFLPHHCDAEALYFVNGCTTFTWHNEKESYANORGVVS	235
QY	302	IPASTPFLYLRDNERNRHLAKLQOTISFGOYKEFRPAGGODERPLSTFSKEIIAAL	361
Db	236	VPAQSTYYVVSQDOQEKTLIVLALPWNSEOKYELFFRPAGNKPDESTYGAFTSEVLTFV	295
QY	362	NYOTERLGVGLGOOR-----EGVILIRASQEOIRELTRDSESRMHILRRGSESSRG	413

Db	296	NTQREKLEELIEEQGGQGRQOQOQGMFRKAKPEQVIRAIISQDATSPR----	HRGGE	-	RLA	349
Qy	414	YMLFHKRPLYSKTKYGOAAEVAEPEDYRLOLDDYVFIININGSMAGPEFTRSTRKYVV				473
Db	350	INLUSQSYVYSQNRQFFECACPEDFSOFQNMDDVAASAKLNGALFYVHYSKATFYVEV				409
Qy	474	ASGEADYEMACPHLSGRHGRGQGGK--RHEEEVEV----	HYEQRARLISKREALIVYLA			525
Db	410	TDGYGYAMACPHLSRQSGSGSGSQRDREDOEESEEEETFEQFOOVKAPLSPGVGFVAPA				469
Qy	526	GHPYVVEVSSGGENLLFLFAFGINAOHNHNFPLAGRENNVLOLEPQAMLAFAASKEVEE				585
Db	470	GHAVTFPASKQDPLVAAFGLNAQNMQRIFLQAG-KNLVRQMDSEAKLSGCVYSKLVDN				528
Qy	586	LFNSODESTFFPGPRQHQHQSQSPRSTKQOQPLVSYILDF				622
Db	529	IFNNPDESYFMFSQQRQGRDGR--RGNPLASIIDF				562

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RESULT 3
FWCNCMB
alpha-globulin B precursor (clone C72) - upland cotton
N:Alternate names: seed storage protein; vicilin precursor
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A30838; S06911
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
P:Plant Mol. Biol. 7, 475-489, 1986
A>Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A:Reference number: A30838
A:Accession: A30838
A:Molecule type: mRNA
A:Residues: 1-588 <CHL>
A:Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A:Experimental source: var. Coker 201
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
P:Plant Mol. Biol. 9, 533-546, 1987
A>Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S06398
A:Accession: S06911
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-81 <CH2>
C:Comment: This is a seed storage protein.
C:Superfamily: glycinin
C:Keywords: glycoprotein; seed; storage protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-588/Product: alpha-globulin storage proprotein #status predicted <Mat>
F:411/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match	32.3%	Score 1074.5	DB 1	Length 588
Best Local Similarity	38.2%	Pred No. 1.6e-60		
Matches 229	Conservative 115	Mismatches 181	Indels 75	Gaps 13

QY	35	EDJTECQCCGRRCRQDSBDRQOQYORCKELCEEENRNR--DPQOQYBQOCRC	92
Db	35	DDPKRYEDCCRRCMDTRGQEQOQCESSQSYGEKDDQQRHPRDPRTEECQEC	94
QY	93	QRRTPEPHMOJCOQRCERYEKEK RKQOQRYEEOQREDEKEYEEMKEGDKNRDPQORE	152
Db	95	--RQEQQRQRCQCCRLKREQEQOQ-----SQRO	123
QY	153	YEDCRHCEQOE--PRLOYQCRQCEQOQONGGGLMNPQ-----GGSGRYEGEE	204
Db	124	FOEQCOHQHOEQOEPERQOQCVRCREYQO-----NPMRREREBEAEEETECEGO	175
QY	205	KQSDMPYCFEDRSJSTRPTEEGHSLVLENGYGRSKLLRALKNYRLILNANPAFLPT	264
Db	176	EOSHNPFFHHRQSQRFEHENGFRVLYQNFASHNPLRLRGINGEIRLSLILBNPPTFLPH	235
QY	265	HLDDADALLVYGGAALKMJHRDNRESYNLECGDVIRIPAGTTFYLLNRNNERTILAFK	324

[illegible]

RESULT 4
S06398
alpha-globulin type A precursor - upland cotton
N:Alternate names: seed storage protein
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S06398
R:Chan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. S
A:Reference number: S06398
A:Accession: S06398
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-605 <CHL>
C:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>

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Query Match      32.0%, Score 1063.5; DB 2; Length 605;
Best Local Similarity 38.0%; Pred. No. 8.2e-60;
Matches 232; Conservative 121; Mismatches 195; Indels 63; Gaps 16;

QY      33  NOEDPOTECQOCQRCRCROQESDPFOQOYTQRCRCETICEEEEYNNRQDPQOQYEDQCKRC 92
      ::::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |
Db      33  SEDDEQOAREDECRKRCOLETTRGOTEDQDCEDSESTQLEKEEQORDGE-DPQRRYQDCQHC 91

QY      93  QRRREPR-HMICOQRCRRYKEKRRQOKKRYEQQREDEKTEERMKEGDNKRDPOOR 151
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      92  QOEEBRLRPH-----CEQSCREQYK-----QQQQQPD-----K 120

QY      152  EYEDCRHGEQEE--PRQYOQRCRCQOQORQHNGSGDLMNQR-GSGRYEEGEEKSD 208
      ::::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |
Db      121  QKEQOQRCQWQEOBPRPERKQOCYKCECRQYOQDPMKGRGENKMKREEBEEESDEGEQOQRN 180

QY      209  NPYEDERSLSRTRETEGHSIVLENFYGRSKLLALNNRYLVLEANPNAFVLPETHIDA 268
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181  NNYEYHRHSFOERDEEGNFVLOREFADKHNLGLNGINEFRLTEANPNFVLPETHIDA 240

QY      269  DALLIVIGRGALMKMIHNDNRESVLMCEGDVYRIAPAGTTPFLINDNNERHIAFQDTI 328
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241  EKITVYVTMGKGVTFVTEHNKESVYMWGVVVRIPAGSTVYLANDNNREKLTITALHPV 300

QY      329  STPGQYKEFFPAGQGNPEPYLSTFSKELTEALANQTERLQGVGIC-----QOQEGYTI 381
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301  NNPGQFQAFPPAGQGNPNQSYLRIFSRELLAEVNTSRQDLDELPGROSRRHQOQOQCFR 360

QY      382  RASQOIRELTTFDSESRWHIRRGESSRG-PYVLFMKRPYLSNKGQAVYEPEDV-R 439

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Db 361 KASQDQIRALISGATSPR-----GKGSBEYAFANLLLSQTTPRSSNONGREYACPRHFOQ 413

QY 440 QIOMDVSVFANTITQSGMGPFFNTSTKVVVYVASEADYEMACPILSRHGGRGGKR 499

Db 414 QIREVDSSVALEINKGSIPEVPHNSKATFVYLVLTGEGNGHEVWCPIILS-RQSDWSRE 472

QY 500 HEEDEEV-----HYEGRARLSKREAVIYLGHPPVAVFSSGNEINLLTFAFI-NAQN 551

Db 473 EEEQEEQEEVERRRSGYKKVRAQLSTGNLFVVPACHPTFVAQNEHDLGLLGFGLYNGDN 552

QY 552 HENFLAGGERIVLOIIEPQAMELAFASRKREVELLEFVSQDESTIFFPQRRHQOQSPRSTK 611

Db 533 KRIYVAGTNNV-RQMDRQAKELAFGVESRLVDEVFNNPQESTFVSGRRKGFDEP-RG 590

QY 612 QOQPLVSTLDF 622

Db 591 SNNPLSPFLDF 601

RESULT 5
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N:Alternate names: seed storage protein
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chian, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX
A:Reference number: S06398
A:Accession: S08059
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-509 <CHL>
C:Superfamily: glycinin

Query Match	30.6%	Score 1018.5	DB 2	length 509
Best Local Similarity	39.1%	Pred. No. 4.6e-57		
Matches 217	Conservative 106	Mismatches 157	Indels 75	Gaps 12
OY	DPQOQYEDCCOKRCQRRTEPRMIHQICQQRCEBRYEKERKROOKRYEEQOREDEEKYEERM	139		
Db	1 DPQRVEEQCGQEC--RQGEERQOPQCGQRCLKRFEEQDQ-----	38		
OY	140 KEGDNKRPDQOHEEDYEDCKRHCEQD--PRLOYOCQRCQEDQROHQRGGDLNPNQRC--	194		
Db	39-----SORQPECCQCHQOQROREKKQOCVCRECREKYO-----NPKRGERE	81		
OY	195---GSGRVEEGCEKQSDPNPYFEDERSLSTRPTEEGHISYLENFYGRSLFALNRYLV	251		
Db	82 EEAESEETEEEGQEQDSNPNFPHHRSPSPSRFEHNGNRVLRQFASRNPILRGINEFRLS	141		
OY	252 LLEANPNAFVLEPTLLDADAILLVIGGRALKMIRHNDRESYNLECGDVIKIPAGTFYELI	311		
Db	142 ILEANPNFVLEPHHODAKELIVLTNGRGLTFLEHNEKESYNIYGVVVKVAGSTVYLLA	201		
OY	312 NRDNNEERHIAKFLQTTITSPGOYKEFFPAGCONPNPPYLSSTSKELLEALNTPQRLGV	371		
Db	202 NQDNKEKILIVLHVRPNVNPQGFEEFFPAGSORPQSYLRATSRLELLEPAFNTRSSQDEL	261		
OY	372 LG-----QOREGVIIINASQEQIRLETRDDSESRHMIIRGGESRGPVLFNKRPLYS	424		
Db	262 FCGRQSRRRQOQCGCFKRAQSOBJALTSQEAFTSPR---EKSGE--RPAFNILSOTPRYS	315		
OY	425 NKTYGAYVEKREDYEROLQDMMVSFVIANITGGSMNGPEFNFNRKRVVVYVAGGEADVENAC	484		
Db	316 NQNGRFEPACPPERRQLDINVTYSAOLDNQJLFEVPIYNSKATFTVILLVTGNGYAEWS	375		
OY	485 PHLSGRHMGGRGGKRRHEEEV-----HYEYQVRAKLSKREAIVYLAGHPVYVSSGN	536		
Db	376 PHLRQSSYYEEEEEDEEEOEEERSSGGYRKIRJSLTSQDILFEVYANPNPTFVASON	435		

QY 581 KEVEELFNSODESTIFFEPPROHQOOSPRSTKQOQPLVSI 620
 DB 598 KDIEMLIKSOSESYFDA--OPQOKEGKNGKRGKPLSSIL 635

RESULT 12

S00566
 convicillin precursor (clone pUC4) - garden pea
 C:Species: Pisum sativum (garden pea)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
 C:Accession: S00566
 R:Bown, D.; Ellis, T.H.N.; Gatehouse, J.A.
 Biochem. J. 251, 717-726, 1988
 A:Title: The sequence of a gene encoding convicillin from pea (Pisum sativum L.) shows t
 A:Reference number: S00566; MUID:88326208
 A:Accession: S00566
 A:Molecule type: DNA
 A:Residues: 1-571 <BOM>
 A:Cross-references: EMBL:X06398; NID:920698; PIDN:CA2695.1; PID:9313670
 A:Note: part of this sequence, including the amino end of the mature protein, was confir
 C:Genetics:
 A:Gene: cvca
 A:Map position: 2
 A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1
 C:Superfamily: glycylin
 F:1-28/Domain: signal sequence #status predicted <Sig>
 F:29-571/Product: convicillin #status experimental <MAT>

Query Match 25.0%; Score 833; DB 2; Length 571;
 Best Local Similarity 33.2%; Pred. No. 2,7e-45;

Matches 208; Conservative 112; Mismatches 193; Indels 114; Gaps 18;

QY 26 IDMSKYNODPQTECCOQCRRCQOQSDPRQOQYCRCKCEEEENRQORDPOQY 85
 DB 25 VTYANYP--EGSETRVPGQREGRQ-----EGKKEKRKGEMPSY 63
 QY 86 EOCCKRCORETEPRHMOICQRCERRRYEKKERKQOK---RYEEOQREDEEYEEEMKE 141
 DB 64 E-----KEENE-----EKOKYRYQREKKEQKQEVQGRGEMWEDEBOVEEEMRG 109
 QY 142 GDNKRPQOREVEDCRHNEQOEPRLOYCQCRQOQOQHGSGDLMNPOGSGRYEE 201
 DB 110 SORREDEER-----ARLHREER--TKRDRRH-----QREGDEERS 145
 QY 202 GEKQSNPYFFEDERSLSTRFTEEGHISYLENFGSKLLRLKRYLLLEANPMAFY 261
 DB 146 SESOEHRNPELFKSNKFLTEFENNGHIRLRQDRKRSDFENLQNRRLVEYRAKPHITF 205
 QY 262 LPTHLADALILVYGRGALMKIHRDNRESYNLECCDVIYIPACTGPFYLLINRDNNEHLTI 321
 DB 206 LPQIHDADLLVNLNGAILTVLSPNDRNSYNLERGDTIKIPAGTISYLVNODDEEDLRY 265
 QY 322 AKLLOTISTPGQYKEFFPAGQNDPEYLSFESKEILEALINTQTERLQVY----- 372
 DB 266 VDEVIIPVNRPGKEFAF--GLSENNKNOYLNGFSKNILEASINTKYETLEKVLLEEOEKRPQ 323
 QY 373 -----GOOREGVIIIASOEFRELTRDSESRMHIRRGSGESRQPYLLFNKRPL 422
 DB 324 QLEDRKRTQOGEERD-ALLVNSREQLLEKLAKSSS---KSLDSEEPFNLRSHPKE 378
 QY 423 YSNKYGAOAEVKEP-DYROLQDMVSYFIANTIQGSMGPFNTRSKVVVAVSGEADVE 481
 DB 379 YSNKPGKLEIFTEPEKKYPOQDODILVSCVEIKKALMLPHYNSRAIVLVLVNMEGNGLE 438
 QY 482 MACPHLSGRHGGGGRKHEEVEEVIH-----QYARLSKREAIYVLGHPVAVSSG 535
 DB 439 IL-----GLKNEQOEREDRKRNNNEVQRYEARLSPGDVYIIPAGHVAISAS 486
 QY 536 NEMLLFAFGINNONNHNENLAGERNVLOQIEPQAMELAFASRKEVEELFNSODESTIF 595

DB 487 NLNLL--GFGIMKNNKRNFLSGSDDNVYSIOENIPYKELTFPGSSQEVNRLINKQOSHF 544
 QY 596 FPG-PROHQOOSPRSTKQOQPLVSI 621
 DB 545 ASAPPEQKEESOR---KRSPLSSILD 568

RESULT 13

JQ1730
 62K sucrose-binding protein precursor - soybean
 C:Species: Glycine max (soybean)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
 C:Accession: JQ1730
 R:Gimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hiltz, W.D.
 Plant Cell 4, 1561-1574, 1992
 A:Title: A 62-kD sucrose binding protein is expressed and localized in tissues active
 A:Reference number: JQ1730; MUID:93104680
 A:Accession: JQ1730
 A:Molecule type: mRNA
 A:Residues: 1-524 <GR1>
 A:Cross-references: GB:I06038; NID:g1431744; PIDN:ABR03894.1; PID:g170064
 C:Superfamily: glycylin
 C:Keywords: sugar transport
 F:1-29/Domain: signal sequence #status predicted <Sig>
 F:30-524/Product: 62K sucrose-binding protein #status predicted <MAT>

Query Match 23.9%; Score 794; DB 2; Length 524;
 Best Local Similarity 33.4%; Pred. No. 7.1e-43;

Matches 191; Conservative 103; Mismatches 176; Indels 102; Gaps 18;

QY 64 RCKEIEEEEEYRNORDPO--QOYEOCKRCQORETEPRHMOICQOQRCERRRYEKKERKQO 121
 DB 27 KCKETEVEE-----DPELVCKHOCQOQOQYTEGDKR---VCLOSCD-RYHRMKEERE 76
 QY 122 KRYEEOQREDEEYEEEMKKGDKRPOOREVEDCRHNEQOEPRLOYCQCRQOQOQRO 181
 DB 77 KOJOETRE-----KKEESRERE-----EEQOEQ 101
 QY 182 HGGSGDLMNPOGSGRYEEGEKQSDNPYPDE-RLSTRFTEEGHISYLENFGSKR 240
 DB 102 H-----EODENPYTFEEDKQDFETRYTEGGRIVLKKTEKSR 140
 QY 241 LRLAKNRYLLLEANPNFVLPTHLDADAILVYGRGALMKIHRDNRESYNLECCDVIY 300
 DB 141 LQGTENFRLALILEARHNTVSPRHFDSEYVFNIGRAVLGLVSESEKTIPLPQDMI 200
 QY 301 RIPAGTTFYILNDDNERLHIA--KFLQITSTPGQYKEFFPAGQNDPEYLSFESKEILE 358
 DB 201 HIPAGTPPLYVNDENDKFLMLHIPVSVSTPGKFEFEFFAPGGRDPESVLSAFSNVLIQ 260
 QY 359 AALNTQTERLQVYGRGALMKIHRDNRESYNLECCDVIYIPACTGPFYLLINRDNNEHLTI 418
 DB 261 AALQTKKLENVFDQONBESSIFRISREOYRALA-PTKSSMWP--GG-SKPOFNITS 316
 QY 419 KRLYSNKYGAOAEVKEPDEYRQ--LQDMVSYFIANTIQGSMGPFNTRSKVVVAVASG 476
 DB 317 KRPTISNGYGRLEVEBPDDKESWILQRLNMLFTNITQRSMTIYNSMARTIALYIDG 376
 QY 477 EADVACPHLSGRHGGGGRKHEEVEEVIH-----QYARLSKREAIYVLGHPVAVSSG 536
 DB 377 RGHLOISCPHMS---SRSSHSHDKSSP-SYHRISSDLKPGWVFPVPGHFPVTIASRK 431
 QY 537 ENLLFAFGINNONNHNENLAGERNVLOQIEPQAMELAF-----AASRK 581
 DB 432 ENLLMTCFEVNAQDKKFFPAGKD-NIVSSLDVAKEALFANIPSEKVNQVFLDLQREK 490
 QY 582 EVEELFN---SODESIFPPGPROHQOQSPRS 609
 DB 491 LIGRLYHLPHKDKKESFPFPFELPREGRRA 522

RESULT 14

